What is claimed is:

1. An isolated polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-34.

2. A fragment of said isolated polynucleotide of claim 1, wherein said fragment comprises a polymorphic site in the polymorphic sequence.

3. An isolated polynucleotide comprising a sequence complementary to one or more of the polymorphic sequences (SEQ ID NOS 1-34) of claim 1.

4. A fragment of said complementary nucleotide sequence of claim 3, wherein said fragment comprises a polymorphic site in the polymorphic sequence.

5. The isolated polynucleotide of any of claims 1 to 4, wherein said polynucleotide is DNA, RNA, cDNA, or mRNA.

6. The isolated polynucleotide of any of claims 1 to 5, wherein at least one single nucleotide polymorphism is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581]

of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33 and position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34.

7. The isolated polynucleotide of claim 6, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19,

[CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33 and [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34.

8. The complement of any of the isolated polynucleotides of claim 7.

9. The isolated polynucleotide of any of claims 1 to 8, wherein the nucleotide comprises part of the *CYP17* gene, the *CYP3A4* gene or the *SRD5A2* gene.

10. A polypeptide encoded by a polynucleotide according to any of claims 1 to 9.

11. An antibody to a polypeptide according to claim 10.

12. The isolated polynucletotide of any of claims 1 to 9, further comprising a detectable label.

13. The isolated polynucleotide of claim 12, wherein said detectable label is selected from the group consisting of fluorophore, radionuclide, peptide, enzyme, antibody and antigen.

14. The isolated polynucleotide of claim 13, wherein said fluorophore is a fluorescent compound is selected from the group consisting of Hoechst

33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633, DRAQ5 and Alexa 488.

15. A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising analysing a biological sample containing nucleic acid obtained from said subject to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID

No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

16. The method according to claim 15, wherein said nucleic acid is DNA, RNA, cDNA or mRNA.

17. The method according to claims 15 or 16, wherein said single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27,

[CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44 and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

18. The method according to claims 15 or 16, wherein said single nucleotide polymorphism is selected from the complement of any of the single nucleotide polymorphisms of claim 17.

19. The method of any of claims 15 to 18, wherein said analysis is accomplished by sequencing, genotyping, fragment analysis, hybridisation, restriction fragment analysis, oligonucleotide ligation or allelle specific PCR.

20. The method of claim 19, wherein the analysis is accomplished by hybridisation, the method comprising the steps of

i) contacting said nucleic acid with an oligonucleotide that hybridises to one or more isolated polynucleotide polymorphic sequence selected from the group consisting of SEQ ID NOS 1-36 and SEQ ID NOS 42-45 or its complement;

ii) determining whether the nucleic acid and said oligonucleotide hybridize;

whereby hybridisation of the nucleic acid to the oligonucleotide indicates the presence of the polymorphic site in the nucleic acid.

21. A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, or predicting an individual's response to a drug, said method comprising adding an antibody to a polypeptide present in a biological sample obtained from said subject which polypeptide is encoded by a polynucleotide selected from the group consisting of SEQ ID NOS 1-36 and SEQ ID NOS 42-45, or the complement thereof, and detecting specific binding of said antibody to said polypeptide.

22. A kit comprising at least one isolated polynucleotide of at least 5 contiguous nucleotides of SEQ ID NOS 1-36 or SEQ ID NOS 42-45, or the complement thereof, and containing at least one single nucleotide polymorphic site associated with a disease, condition or disorder related to prostate or breast cancer, together with instructions for the use thereof for detecting the presence or the absence of said at least single nucleotide polymorphism in said nucleic acid.

23. An oligonucleotide array comprising at least one oligonucleotide capable of hybridising to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide comprises a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-36 or SEQ ID NOS 42-45.

24. The oligonucleotide array according to claim 23, wherein said first polynucleotide comprises a fragment of any of said nucleotide sequences, said fragment comprising a polymorphic site in said polymorphic sequence.

25. The oligonucleotide array according to claim 23 wherein the first polynucleotide is a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences of SEQ ID NOS 1-36 or SEQ ID NOS 42-45.

26. The oligonucleotide array according to claim 25, wherein the first polynucleotide comprises a fragment of said complementary sequence, said fragment comprising a polymorphic site in said polymorphic sequence.

27. The kit of claim 22 or the array of any of claims 23 to 26, wherein the position of said polymorphic site is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID

No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

28. The kit of claim 22 or the array of claim 27, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5'

region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44 and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

29. The kit of claim 28 or the array of claim 27, wherein at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms of claim 28.

30. The kit of claim 22 or 27 to 29 or the array of any of claims 23 to 29, wherein said oligonucleotide further comprises a detectable label.

31. The kit of claim 30 or the array of claim 30, wherein said label is selected from the group consisting of of fluorophore, radionuclide, peptide, enzyme, antibody or antigen.

32. The kit of claim 30 or the array of claim 30, wherein said fluorophore is a fluorescent compound selected from the group consisting of Hoechst 33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633 DRAQ5 and Alexa 488.

33. A method of treatment or prophylaxis of a subject comprising the steps of

i) analysing a biological sample containing nucleic acid obtained from said subject to detect the presence or absence of at least one single nucleotide polymorphism in SEQ ID NOS 1-36 or SEQ ID NOS 42-45, or the complement thereof, associated with a disease, condition or disorder related to prostate or breast cancer; and

ii) treating the subject for said disease, condition or disorder if step i) detects the presence of at least one single nucleotide polymorphism

in SEQ ID NOS: 1-36 or SEQ ID NOS 42-45, or the complement thereof.

34. The method of claim 33, wherein said nucleic acid is selected from the group consisting of DNA, RNA and mRNA.

35. The method of claims 33 or 34, wherein the sample is analysed to detect the presence or absence of at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31,

position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

36. The method of claim 35, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base

pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

37. The method of claim 35, wherein at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms of claim 36.

38. The method of any of claims 33 to 37, wherein said method counteracts the effect of said at least one single nucleotide polymorphism detected.

39. The method of claims 33 to 38, wherein the method comprises treatment with a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS 1-36 and SEQ ID NOS 42-45, or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14,

position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

40. The method of claim 39, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11,

[CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

41. The method of claim 39, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism which is the complement of any of the single nucleotide polymorphisms of claim 40.

42. The method of any of claims 33 to 38, wherein said method comprises treatment with a polypeptide which is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS 1-36 and SEQ ID NOS 42-45 or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position

[CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44, and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

43. The method of claim 42, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

44. The method of claim 42, wherein the polymorphic sequence does not contain at least one single nucleotide which is the complement of any of the single nucleotide polymorphisms of claim 43.

45. The method of claims 33 to 38, wherein said method comprises treatment with an antibody that binds specifically with a polypeptide encoded by a polynucleotide selected from the group consisting of SEQ ID NOS 1-36 and SEQ ID NOS 42-45, or the complement thereof.

46. A method for predicting the genetic ability of a subject or an organism to metabolise a chemical, said method comprising analysing a biological sample containing nucleic acid obtained from said subject or organism to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488]

of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45,
wherein the presence of a polymorphism at one or more of said positions is indicative of the subject's or organism's ability or inability to metabolise said chemical.

47. The method of claim 46, wherein said analysis comprises detecting or absence of one or more single nucleotide polymorphisms selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of

SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, and [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

48. The method of either of claims 46 or 47, wherein the method further comprises predicting the response of the subject to the chemical by their ability or inability to metabolise the chemical.

49. The method according to any of claims 46 to 48, wherein said chemical is a drug or a xenobiotic.

50. The method according to any of claims 46 to 49, wherein said organism is selected from the group consisting of bacterium, fungus, protozoa, alga, fish, plant, insect and mammal.

51. A vector comprising a polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-36 or SEQ ID NOS 42-45.

52. A host cell transformed with the vector of claim 51.

53. The host cell of claim 52, wherein said host cell is selected from the group consisting of bacterium, fungus, protozoa, alga, fish, plant, insect and mammal.

54. The host cell of claim 53, wherein said mammal cell is a human cell.

55. Method of metabolising a chemical using the host cell of either of claims 52 or 53.

56. Method for making a host cell resistant to a chemical, said method comprising transforming said cell with any of the polynucleotides of claims 1 to 9 or with any of the vectors of claim 51.

57. An isolated haplotype selected from the group consisting of CYP3A4_Hap4 and SRD52_Hap3.

58. The isolated CYP3A4_Hap4 haplotype of Claim 57 wherein said haplotype comprises Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

59. The isolated SRD52_Hap3 haplotype of Claim 57 wherein said haplotype comprises Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at [SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].

60. A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising analysing a biological sample obtained from said subject to detect the presence or absence of a haplotype as defined in any of claims 57-59.

61. A method of diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising adding an antibody to a polypeptide present in a sample obtained from said subject which polypeptide is encoded by a haplotype as defined in any of claims 57-59, or the complement thereof, and detecting specific binding of said antibody to said polypeptide.

62. A method of treatment or prophylaxis of a subject comprising the steps of

i) analysing a sample of biological material containing a nucleic acid obtained from said subject to detect the presence or absence of at least one haplotype as defined in any of claims 57-59, or the complement thereof, associated with a disease, condition or disorder related to prostate or breast cancer; and

ii) treating the subject for said disease, condition or disorder if step i) detects the presence of at least one said haplotype, or the complement thereof.

63. The method of claim 62 wherein the method comprises treatment with a portion of the isolated CYP3A4_Hap4 haplotype according to claim 58 wherein said portion of said haplotype does not consist of at least one allele from the group consisting of Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

64. The method of claim 62 wherein the method comprises treatment with a portion of the isolated SRD5A2_Hap3 haplotype of Claim 59 wherein said portion of said haplotype does not comprise of at least one allele from the group consisting of Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at [SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].